AMENDMENTS TO THE SPECIFICATION

Please insert the following paragraphs after line 2 on page 1:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 60/372,450, filed on April 16, 2002.

Please replace the Paragraph on page 1 starting on line 6 with the following paragraph rewritten in amendment format:

TB is a deadly contagious disease caused by the infectious agent, *Mycobacteriu tuberculosis*. It kills 2 million people each year. The World Health Organization (WHO) 2001 annual report estimated that there would be 8. 4 million new TB cases in 1999, up from 8.0 million in 1997. If the present trend continues, it is estimated that between 2000 and 2020, nearly one billion people will be newly infected, 200 million people will become ill and 35 million will die from TB. The spread of HIV/AIDS and the emergence of multidrug-resistant TB contribute to the worsening impact of this disease. Bacille Calmette-Guerin (BCG), an attenuated strain of *Mycobacterium bovis*, is currently the only available vaccine for the prevention of TB. In animal models of infection, BCG vaccination has been demonstrated to induce protective immunity against a M tuberculosis challenge (~~Baldwins~~ Baldwin et al., 1998). In humans, BCG vaccination has demonstrated consistent protection against the childhood forms of TB, especially meningitis. However, BCG vaccination is controversial due to variations in its efficacy for protecting adults from pulmonary TB (Fine, 1989; Colditz et al. , 1994; Sterne et al. ,

1998). Trials conducted in the 1940s and 1950s in developed countries such as the United Kingdom, Denmark and North America demonstrated the vaccine to be highly efficient (70-80%). However, in the single largest clinical trial, which took place inIndia in 1970s and involved more than 265,000 persons, BCG vaccination provided no detectable protection against pulmonary TB. Thus, there is an urgent need to generate an improved vaccine(s) to replace the BCG and to prevent TB.

Please replace the Paragraph on page 8 starting on line 16 with the following paragraph rewritten in amendment format:

Fig. 3. Inhibition of BCG growth by L-alanine in GAS. BCG-Japan, BCG-Frappier, and BCG-Pasteur grown to stationary phase in7H9/ADC/glycerol/Tween-80 liquid media, were each inoculated into ~~duplicated~~ duplicate 5 ml culture volumes of GAS, GAS without L-alanine, and GAS supplemented with 27 mM L-asparagine, to a cell densityof 2 x107 cells/ml. Cultures were incubated at37 C with constant shaking for 16 days and then 2 ml aliquots of cell culture were centrifuged and cell pellet lyophilized to determine cell dry weight.

Please replace the Paragraph on page 14 starting on line 3 with the following paragraph rewritten in amendment format:

Nucleic acid molecules may encode conservative amino acid changes in alanine dehydrogenase, glutamine synthetase or L-serine dehydratase. The invention includes functionally equivalent nucleic acid molecules that encode conservative amino acid changes within alanine dehydrogenase, glutamine synthetase or L-serine dehydratase

and produce silent amino acid changes in alanine dehydrogenase, glutamine synthetase or L- serine dehydratase. Methods for identifying empirically conserved amino acid substitution groups are well known in the art (see for example, Wu, Thomas D. "Discovering Emperically Conserved Amino Acid Substitution Groups in Databases of Protein Families" (~~http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list~uids=8877523&dopt=Abstract~~).

Please replace the Paragraph on page 15 starting on line 14 with the following paragraph rewritten in amendment format:

Sequence identity (each construct preferably without a coding nucleic acid molecule insert) is preferably set at least about: 70% identity, at least 80% identity, at least 90% identity, at least 95% identity, at least 96% identity, at least 97% identity, at least 98% identity or, most preferred, at least 99% or 99.5% identity to the sequences provided in SEQ ID NO : 1 to SEQ ID NO : 14 or its complementary sequence). Sequence identity will preferably be calculated with the GCG program from Bioinformatics (University of Wisconsin). Other programs are also available to calculate sequence identity, such as the Clustal W program (preferably using default parameters ; Thompson, JD et al. , Nucleic Acid Res. 22: 4673-4680), BLAST P, BLAST X algorithms, Mycobacterium avium BLASTN at The Institute for Genomic Research (~~http:tigrblast.tigr.org/~~), Mycobacterium bovis, M. Bovis BCG (Pastuer), M. marinum, M. leprae, M. tuberculosis BLASTN at the Wellcome Trust Sanger Institute (~~http://www.sanger.ac.uk/Projects/Microbes/~~), M. tuberculosis BLAST searches at

Institute Pasterur (Tuberculist) ~~(http://genolist.pasteur.fr/TubercuList/)~~, M. leprae BLAST searches at Institute Pasteur (Leproma) ~~(http://genolist.pasteur.fr/Leproma/)~~, M. Paratuberculosis BLASTN at Microbial Genome Project, University of Minnesota ~~(http://www.cbc.umn.edu/ResearchProjects/Ptb/~~ and ~~(http://www.cbc.umn.edu/ResearchProjects/AGAC/MptbAMptbhome.html)~~,various BLAST searches at the National Center for Biotechnology Information-USA ~~(http://ncbi.nlm.nih.gov/BLAST/)~~ and various BLAST searches at GenomeNet(Bioinformatics Center-Institute for Chemical Research) ~~(http://blast.genome.ad.jp/)~~.

Please replace the Paragraph on page 20 starting on line 1 with the following paragraph rewritten in amendment format:

The pharmaceutical compositions of this invention are used for the ~~treatmentment~~ treatment or prophylaxis of a mammal against challenge by *Mycobacterium tuberculosis* or *Mycobacterium bovis*. The pharmaceutical compositions of this invention are also used to treat patients having degenerative diseases, disorders or abnormal physical states such as cancer.